

SEQUENCE LISTING

<110> Edwin L. Madison
Edgar O. Ong

<120> NUCLEIC ACID MOLECULES ENCODING TRANSMEMBRANE SERINE PROTEASE 7, THE
ENCODED POLYPEPTIDES AND METHODS BASED THEREON

<130> 24745-1613

<140>

<141> Herewith

<150> 60/275,592

<151> 2001-03-13

<160> 22

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3147

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (23)...(2589)

<223> Nucleotide sequence encoding MTSP1

<300>

<301> O'Brien, T.J. and Tanimoto, H.

<308> GenBank #AR081724

<309> 2000-08-31

<310> 5,972,616

<311> 1998-02-20

<312> 1999-10-26

<400> 1

tcaagagcgg cctcggggta cc atg ggg agc gat cgg gcc cgc aag ggc gga	52
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly	
1 5 10	
ggg ggc ccg aag gac ttc ggc gcg gga ctc aag tac aac tcc cgg cac	100
Gly Gly Pro Lys Asp Phe Gly Ala Gly Leu Lys Tyr Asn Ser Arg His	
15 20 25	
gag aaa gtg aat ggc ttg gag gaa ggc gtg gag ttc ctg cca gtc aac	148
Glu Lys Val Asn Gly Leu Glu Glu Gly Val Glu Phe Leu Pro Val Asn	
30 35 40	
aac gtc aag aag gtg gaa aag cat ggc ccg ggg cgc tgg gtg gtg ctg	196
Asn Val Lys Lys Val Glu Lys His Gly Pro Gly Arg Trp Val Val Leu	
45 50 55	
gca gcc gtg ctg atc ggc ctc ctc ttg gtc ttg ctg ggg atc ggc ttc	244
Ala Ala Val Leu Ile Gly Leu Leu Leu Val Leu Leu Gly Ile Gly Phe	
60 65 70	
ctg gtg tgg cat ttg cag tac cgg gac gtg cgt gtc cag aag gtc ttc	292
Leu Val Trp His Leu Gln Tyr Arg Asp Val Arg Val Gln Lys Val Phe	

24745-1613

75	80	85	90	
aat ggc tac atg agg atc aca aat gag aat ttt gtg gat gcc tac gag Asn Gly Tyr Met Arg Ile Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu	95	100	105	340
aac tcc aac tcc act gag ttt gta agc ctg gcc agc aag gtg aag gac Asn Ser Asn Ser Thr Glu Phe Val Ser Leu Ala Ser Lys Val Lys Asp	110	115	120	388
gcg ctg aag ctg ctg tac agc gga gtc cca ttc ctg gcc ccc tac cac Ala Leu Lys Leu Leu Tyr Ser Gly Val Pro Phe Leu Gly Pro Tyr His	125	130	135	436
aag gag tcg gct gtg acg gcc ttc agc gag gcc agc gtc atc gcc tac Lys Glu Ser Ala Val Thr Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr	140	145	150	484
tac tgg tct gag ttc agc atc ccg cag cac ctg gtg gag gag gcc gag Tyr Trp Ser Glu Phe Ser Ile Pro Gln His Leu Val Glu Glu Ala Glu	155	160	165	532
cgc gtc atg gcc gag gag cgc gta gtc atg ctg ccc ccg cgg gcg cgc Arg Val Met Ala Glu Glu Arg Val Val Met Leu Pro Pro Arg Ala Arg	175	180	185	580
tcc ctg aag tcc ttt gtg gtc acc tca gtg gtg gct ttc ccc acg gac Ser Leu Lys Ser Phe Val Val Thr Ser Val Val Ala Phe Pro Thr Asp	190	195	200	628
tcc aaa aca gta cag agg acc cag gac aac agc tgc agc ttt gcc ctg Ser Lys Thr Val Gln Arg Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu	205	210	215	676
cac gcc cgc ggt gtg gag ctg atg cgc ttc acc acg ccc gcc ttc cct His Ala Arg Gly Val Glu Leu Met Arg Phe Thr Thr Pro Gly Phe Pro	220	225	230	724
gac agc ccc tac ccc gct cat gcc cgc tgc cag tgg gcc ctg cgg ggg Asp Ser Pro Tyr Pro Ala His Ala Arg Cys Gln Trp Ala Leu Arg Gly	235	240	245	772
gac gcc gac tca gtg ctg agc ctc acc ttc cgc agc ttt gac ctt gcg Asp Ala Asp Ser Val Leu Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala	255	260	265	820
tcc tgc gac gag cgc gcc agc gac ctg gtg acg gtg tac aac acc ctg Ser Cys Asp Glu Arg Gly Ser Asp Leu Val Thr Val Tyr Asn Thr Leu	270	275	280	868
agc ccc atg gag ccc cac gcc ctg gtg cag ttg tgt gcc acc tac cct Ser Pro Met Glu Pro His Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro	285	290	295	916
ccc tcc tac aac ctg acc ttc cac tcc tcc cag aac gtc ctg ctc atc Pro Ser Tyr Asn Leu Thr Phe His Ser Ser Gln Asn Val Leu Leu Ile	300	305	310	964
aca ctg ata acc aac act gag cgg cgg cat ccc gcc ttt gag gcc acc Thr Leu Ile Thr Asn Thr Glu Arg Arg His Pro Gly Phe Glu Ala Thr	315	320	325	1012

24745-1613

ttc ttc cag ctg cct agg atg agc agc tgt gga ggc cgc tta cgt aaa Phe Phe Gln Leu Pro Arg Met Ser Ser Cys Gly Gly Arg Leu Arg Lys 335 340 345	1060
gcc cag ggg aca ttc aac agc ccc tac tac cca ggc cac tac cca ccc Ala Gln Gly Thr Phe Asn Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro 350 355 360	1108
aac att gac tgc aca tgg aac att gag gtg ccc aac aac cag cat gtg Asn Ile Asp Cys Thr Trp Asn Ile Glu Val Pro Asn Asn Gln His Val 365 370 375	1156
aag gtg agc ttc aaa ttc ttc tac ctg ctg gag ccc ggc gtg cct gcg Lys Val Ser Phe Lys Phe Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala 380 385 390	1204
ggc acc tgc ccc aag gac tac gtg gag atc aat ggg gag aaa tac tgc Gly Thr Cys Pro Lys Asp Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys 395 400 405 410	1252
gga gag agg tcc cag ttc gtc gtc acc agc aac agc aac aag atc aca Gly Glu Arg Ser Gln Phe Val Val Thr Ser Asn Ser Asn Lys Ile Thr 415 420 425	1300
gtt cgc ttc cac tca gat cag tcc tac acc gac acc ggc ttc tta gct Val Arg Phe His Ser Asp Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala 430 435 440	1348
gaa tac ctc tcc tac gac tcc agt gac cca tgc ccg ggg cag ttc acg Glu Tyr Leu Ser Tyr Asp Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr 445 450 455	1396
tgc cgc acg ggg cgg tgt atc cgg aag gag ctg cgc tgt gat ggc tgg Cys Arg Thr Gly Arg Cys Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp 460 465 470	1444
gcc gac tgc acc gac cac agc gat gag ctc aac tgc agt tgc gac gcc Ala Asp Cys Thr Asp His Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala 475 480 485 490	1492
ggc cac cag ttc acg tgc aag aac aag ttc tgc aag ccc ctc ttc tgg Gly His Gln Phe Thr Cys Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp 495 500 505	1540
gtc tgc gac agt gtg aac gac tgc gga gac aac agc gac gag cag ggg Val Cys Asp Ser Val Asn Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly 510 515 520	1588
tgc agt tgt ccg gcc cag acc ttc agg tgt tcc aat ggg aag tgc ctc Cys Ser Cys Pro Ala Gln Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu 525 530 535	1636
tcg aaa agc cag cag tgc aat ggg aag gac gac tgt ggg gac ggg tcc Ser Lys Ser Gln Gln Cys Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser 540 545 550	1684
gac gag gcc tcc tgc ccc aag gtg aac gtc gtc act tgt acc aaa cac Asp Glu Ala Ser Cys Pro Lys Val Asn Val Val Thr Cys Thr Lys His 555 560 565 570	1732

24745-1613

acc tac cgc tgc ctc aat ggg ctc tgc ttg agc aag ggc aac cct gag	1780
Thr Tyr Arg Cys Leu Asn Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu	
575 580 585	
tgt gac ggg aag gag gac tgt agc gac ggc tca gat gag aag gac tgc	1828
Cys Asp Gly Lys Glu Asp Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys	
590 595 600	
gac tgt ggg ctg cgg tca ttc acg aga cag gct cgt gtt gtt ggg ggc	1876
Asp Cys Gly Leu Arg Ser Phe Thr Arg Gln Ala Arg Val Val Gly Gly	
605 610 615	
acg gat gcg gat gag ggc gag tgg ccc tgg cag gta agc ctg cat gct	1924
Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val Ser Leu His Ala	
620 625 630	
ctg ggc cag ggc cac atc tgc ggt gct tcc ctc atc tct ccc aac tgg	1972
Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp	
635 640 645 650	
ctg gtc tct gcc gca cac tgc tac atc gat gac aga gga ttc agg tac	2020
Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr	
655 660 665	
tca gac ccc acg cag tgg acg gcc ttc ctg ggc ttg cac gac cag agc	2068
Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu His Asp Gln Ser	
670 675 680	
cag cgc agc gcc cct ggg gtg cag gag cgc agg ctc aag cgc atc atc	2116
Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu Lys Arg Ile Ile	
685 690 695	
tcc cac ccc ttc ttc aat gac ttc acc ttc gac tat gac atc gcg ctg	2164
Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu	
700 705 710	
ctg gag ctg gag aaa ccg gca gag tac agc tcc atg gtg cgg ccc atc	2212
Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met Val Arg Pro Ile	
715 720 725 730	
tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc ggc aag gcc atc tgg	2260
Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly Lys Ala Ile Trp	
735 740 745	
gtc acg ggc tgg gga cac acc cag tat gga ggc act ggc gcg ctg atc	2308
Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile	
750 755 760	
ctg caa aag ggt gag atc cgc gtc atc aac cag acc acc tgc gag aac	2356
Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr Thr Cys Glu Asn	
765 770 775	
ctc ctg ccg cag cag atc acg ccg cgc atg atg tgc gtg ggc ttc ctc	2404
Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys Val Gly Phe Leu	
780 785 790	
agc ggc ggc gtg gac tcc tgc cag ggt gat tcc ggg gga ccc ctg tcc	2452
Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser	
795 800 805 810	
agc gtg gag gcg gat ggg cgg atc ttc cag gcc ggt gtg gtg agc tgg	2500

[illegible]

```
<210> 2
<211> 855
<212> PRT
<213> Homo Sapien
```

<400>	2															
Met	Gly	Ser	Asp	Arg	Ala	Arg	Lys	Gly	Gly	Gly	Gly	Pro	Lys	Asp	Phe	
1				5					10					15		
Gly	Ala	Gly	Leu	Lys	Tyr	Asn	Ser	Arg	His	Glu	Lys	Val	Asn	Gly	Leu	
			20					25					30			
Glu	Glu	Gly	Val	Glu	Phe	Leu	Pro	Val	Asn	Asn	Val	Lys	Lys	Val	Glu	
		35					40					45				
Lys	His	Gly	Pro	Gly	Arg	Trp	Val	Val	Leu	Ala	Ala	Val	Leu	Ile	Gly	
	50					55				60						
Leu	Leu	Leu	Val	Leu	Leu	Gly	Ile	Gly	Phe	Leu	Val	Trp	His	Leu	Gln	
65					70				75						80	
Tyr	Arg	Asp	Val	Arg	Val	Gln	Lys	Val	Phe	Asn	Gly	Tyr	Met	Arg	Ile	
				85					90					95		
Thr	Asn	Glu	Asn	Phe	Val	Asp	Ala	Tyr	Glu	Asn	Ser	Asn	Ser	Thr	Glu	
			100					105					110			
Phe	Val	Ser	Leu	Ala	Ser	Lys	Val	Lys	Asp	Ala	Leu	Lys	Leu	Leu	Tyr	
		115					120					125				
Ser	Gly	Val	Pro	Phe	Leu	Gly	Pro	Tyr	His	Lys	Glu	Ser	Ala	Val	Thr	
	130					135					140					
Ala	Phe	Ser	Glu	Gly	Ser	Val	Ile	Ala	Tyr	Tyr	Trp	Ser	Glu	Phe	Ser	
145					150					155					160	
Ile	Pro	Gln	His	Leu	Val	Glu	Glu	Ala	Glu	Arg	Val	Met	Ala	Glu	Glu	
				165					170					175		
Arg	Val	Val	Met	Leu	Pro	Pro	Arg	Ala	Arg	Ser	Leu	Lys	Ser	Phe	Val	
			180					185					190			
Val	Thr	Ser	Val	Val	Ala	Phe	Pro	Thr	Asp	Ser	Lys	Thr	Val	Gln	Arg	
		195					200					205				
Thr	Gln	Asp	Asn	Ser	Cys	Ser	Phe	Gly	Leu	His	Ala	Arg	Gly	Val	Glu	
	210					215					220					
Leu	Met	Arg	Phe	Thr	Thr	Pro	Gly	Phe	Pro	Asp	Ser	Pro	Tyr	Pro	Ala	
225					230					235					240	
His	Ala	Arg	Cys	Gln	Trp	Ala	Leu	Arg	Gly	Asp	Ala	Asp	Ser	Val	Leu	
				245					250					255		
Ser	Leu	Thr	Phe	Arg	Ser	Phe	Asp	Leu	Ala	Ser	Cys	Asp	Glu	Arg	Gly	

			260					265					270			
Ser	Asp	Leu	Val	Thr	Val	Tyr	Asn	Thr	Leu	Ser	Pro	Met	Glu	Pro	His	
		275					280					285				
Ala	Leu	Val	Gln	Leu	Cys	Gly	Thr	Tyr	Pro	Pro	Ser	Tyr	Asn	Leu	Thr	
	290					295					300					
Phe	His	Ser	Ser	Gln	Asn	Val	Leu	Leu	Ile	Thr	Leu	Ile	Thr	Asn	Thr	
305					310					315					320	
Glu	Arg	Arg	His	Pro	Gly	Phe	Glu	Ala	Thr	Phe	Phe	Gln	Leu	Pro	Arg	
			325					330						335		
Met	Ser	Ser	Cys	Gly	Gly	Arg	Leu	Arg	Lys	Ala	Gln	Gly	Thr	Phe	Asn	
			340					345					350			
Ser	Pro	Tyr	Tyr	Pro	Gly	His	Tyr	Pro	Pro	Asn	Ile	Asp	Cys	Thr	Trp	
		355					360					365				
Asn	Ile	Glu	Val	Pro	Asn	Asn	Gln	His	Val	Lys	Val	Ser	Phe	Lys	Phe	
	370					375						380				
Phe	Tyr	Leu	Leu	Glu	Pro	Gly	Val	Pro	Ala	Gly	Thr	Cys	Pro	Lys	Asp	
385					390					395					400	
Tyr	Val	Glu	Ile	Asn	Gly	Glu	Lys	Tyr	Cys	Gly	Glu	Arg	Ser	Gln	Phe	
				405					410					415		
Val	Val	Thr	Ser	Asn	Ser	Asn	Lys	Ile	Thr	Val	Arg	Phe	His	Ser	Asp	
			420					425					430			
Gln	Ser	Tyr	Thr	Asp	Thr	Gly	Phe	Leu	Ala	Glu	Tyr	Leu	Ser	Tyr	Asp	
		435					440					445				
Ser	Ser	Asp	Pro	Cys	Pro	Gly	Gln	Phe	Thr	Cys	Arg	Thr	Gly	Arg	Cys	
	450					455					460					
Ile	Arg	Lys	Glu	Leu	Arg	Cys	Asp	Gly	Trp	Ala	Asp	Cys	Thr	Asp	His	
465					470					475					480	
Ser	Asp	Glu	Leu	Asn	Cys	Ser	Cys	Asp	Ala	Gly	His	Gln	Phe	Thr	Cys	
				485					490					495		
Lys	Asn	Lys	Phe	Cys	Lys	Pro	Leu	Phe	Trp	Val	Cys	Asp	Ser	Val	Asn	
			500					505					510			
Asp	Cys	Gly	Asp	Asn	Ser	Asp	Glu	Gln	Gly	Cys	Ser	Cys	Pro	Ala	Gln	
		515					520					525				
Thr	Phe	Arg	Cys	Ser	Asn	Gly	Lys	Cys	Leu	Ser	Lys	Ser	Gln	Gln	Cys	
	530					535					540					
Asn	Gly	Lys	Asp	Asp	Cys	Gly	Asp	Gly	Ser	Asp	Glu	Ala	Ser	Cys	Pro	
545					550					555					560	
Lys	Val	Asn	Val	Val	Thr	Cys	Thr	Lys	His	Thr	Tyr	Arg	Cys	Leu	Asn	
				565					570					575		
Gly	Leu	Cys	Leu	Ser	Lys	Gly	Asn	Pro	Glu	Cys	Asp	Gly	Lys	Glu	Asp	
			580					585					590			
Cys	Ser	Asp	Gly	Ser	Asp	Glu	Lys	Asp	Cys	Asp	Cys	Gly	Leu	Arg	Ser	
		595					600									

24745-1613

Thr	Gln	Tyr	Gly	Gly	Thr	Gly	Ala	Leu	Ile	Leu	Gln	Lys	Gly	Glu	Ile
		755					760					765			
Arg	Val	Ile	Asn	Gln	Thr	Thr	Cys	Glu	Asn	Leu	Leu	Pro	Gln	Gln	Ile
	770					775					780				
Thr	Pro	Arg	Met	Met	Cys	Val	Gly	Phe	Leu	Ser	Gly	Gly	Val	Asp	Ser
785					790					795					800
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Ser	Ser	Val	Glu	Ala	Asp	Gly
				805					810					815	
Arg	Ile	Phe	Gln	Ala	Gly	Val	Val	Ser	Trp	Gly	Asp	Gly	Cys	Ala	Gln
			820					825					830		
Arg	Asn	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Leu	Pro	Leu	Phe	Arg	Asp	Trp
	835						840					845			
Ile	Lys	Glu	Asn	Thr	Gly	Val									
	850					855									

<210> 3

<211> 3147

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (1865)...(2590)

<223> Nucleic acid sequence of protease domain of MTSP1

<400> 3

tcaagagcgg	cctcgggggta	ccatgggggag	cgatcggggcc	cgcaagggcg	gaggggggccc	60
gaaggacttc	ggcgcgggac	tcaagtacaa	ctcccggcac	gagaaagtga	atggcttgga	120
ggaaggcgtg	gagttcctgc	cagtcaacaa	cgtcaagaag	gtggaaaagc	atggcccggg	180
gcgctgggtg	gtgctggcag	ccgtgctgat	cggcctcctc	ttgggtcttg	tggggatcgg	240
cttcctgggtg	tggcatttgc	agtaccggga	cgtgcgtgtc	cagaaggtct	tcaatggcta	300
catgaggatc	acaaatgaga	atthttgtgga	tgcctacgag	aactccaact	ccactgagtt	360
tgtaagcctg	gccagcaagg	tgaaggacgc	gctgaagctg	ctgtacagcg	gagtcccatt	420
cctggggccc	taccacaagg	agtcggctgt	gacggccttc	agcgagggca	gcgtcatcgc	480
ctactactgg	tctgagttca	gcatcccgc	gcacctgggtg	gaggaggccg	agcgcgatcat	540
ggccgaggag	cgcgtagtca	tgctgcccc	gcgggcgcg	tcctgaagt	cctttgtggt	600
cacctcagtg	gtggctttcc	ccacggactc	caaaacagta	cagaggaccc	aggacaacag	660
ctgcagcttt	ggcctgcacg	cccgcggtgt	ggagctgatg	cgcttcacca	cgcccggctt	720
ccctgacagc	ccctacccc	ctcatgccc	ctgccagtg	gccctgcggg	gggacgccga	780
ctcagtgctg	agcctcacct	tccgcagctt	tgaccttg	tcctgacg	agcgcgag	840
cgacctgggtg	acggtgtaca	acacctgag	ccccatggag	ccccacgccc	tggtgcagtt	900
gtgtggcacc	tacctccct	cctacaacct	gaccttcac	tcctcccaga	acgtcctgct	960
catcacactg	ataaccaaca	ctgagcggcg	gcatcccggc	tttgaggcca	ccttcttcca	1020
gctgcctagg	atgagcagct	gtggaggccg	cttacgtaaa	gcccagggga	cattcaacag	1080
cccctactac	ccaggccact	acccacccaa	cattgactgc	acatggaaca	ttgaggtgcc	1140
caacaaccag	catgtgaagg	tgagcttcaa	attcttctac	ctgctggagc	ccggcggtgcc	1200
tgcgggcacc	tgccccaagg	actacgtgga	gatcaatggg	gagaaatact	gcggagagag	1260
gtcccagttc	gtcgtcacca	gcaacagcaa	caagatcaca	gttcgcttcc	actcagatca	1320
gtcctacacc	gacaccggct	tcttagctga	atacctctcc	tacgactcca	gtgacccatg	1380
cccggggcag	ttcacgtgcc	gcacggggcg	gtgtatccgg	aaggagctgc	gctgtgatgg	1440
ctggggccgac	tgcaccgacc	acagcgatga	gctcaactgc	agttgcgacg	ccggccacca	1500
gttcacgtgc	aagaacaagt	tctgcaagcc	cctcttctgg	gtctgcgaca	gtgtgaacga	1560
ctgcggagac	aacagcgacg	agcaggggtg	cagttgtccg	gcccagacct	tcaggtgttc	1620
caatgggaag	tgctctcga	aaagccagca	gtgcaatggg	aaggacgact	gtggggacgg	1680
gtccgacgag	gcctcctgcc	ccaaggtgaa	cgtcgtcact	tgtaccaa	acacctaccg	1740
ctgcctcaat	gggctctgct	tgagcaaggg	caaccctgag	tgtgacggga	aggaggactg	1800
tagcgacggc	tcagatgaga	aggactgcga	ctgtgggctg	cggtcattca	cgagacaggc	1860
tcgt gtt gtt ggg ggc	acg gat gcg	gat gag ggc	gat gag ggc	gat gag ggc	gat gag ggc	1909
Val Val Gly Gly Thr Asp Ala	Asp Glu Gly Glu Trp Pro Trp Gln					
1	5	10	15			

24745-1613

gta agc ctg cat gct ctg ggc cag ggc cac atc tgc ggt gct tcc ctc Val Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu 20 25 30	1957
atc tct ccc aac tgg ctg gtc tct gcc gca cac tgc tac atc gat gac Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp 35 40 45	2005
aga gga ttc agg tac tca gac ccc acg cag tgg acg gcc ttc ctg ggc Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly 50 55 60	2053
ttg cac gac cag agc cag cgc agc gcc cct ggg gtg cag gag cgc agg Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg 65 70 75	2101
ctc aag cgc atc atc tcc cac ccc ttc ttc aat gac ttc acc ttc gac Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp 80 85 90 95	2149
tat gac atc gcg ctg ctg gag ctg gag aaa ccg gca gag tac agc tcc Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser 100 105 110	2197
atg gtg cgg ccc atc tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala 115 120 125	2245
ggc aag gcc atc tgg gtc acg ggc tgg gga cac acc cag tat gga ggc Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly 130 135 140	2293
act ggc gcg ctg atc ctg caa aag ggt gag atc cgc gtc atc aac cag Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln 145 150 155	2341
acc acc tgc gag aac ctc ctg ccg cag cag atc acg ccg cgc atg atg Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met 160 165 170 175	2389
tgc gtg ggc ttc ctc agc ggc ggc gtg gac tcc tgc cag ggt gat tcc Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser 180 185 190	2437
ggg gga ccc ctg tcc agc gtg gag gcg gat ggg ccg atc ttc cag gcc Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala 195 200 205	2485
ggt gtg gtg agc tgg gga gac ggc tgc gct cag agg aac aag cca ggc Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly 210 215 220	2533
gtg tac aca agg ctc cct ctg ttt cgg gac tgg atc aaa gag aac act Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr 225 230 235	2581
ggg gta tag gggccggggc caccctaatg tgtacacctg cggggccacc Gly Val * 240	2630
catcgtccac ccagtggtgc acgcctgcag gctggagact ggaccgctga ctgcaccagc	2690

24745-1613

```

gccccagaa catacactgt gaactcaatc tccagggctc caaatctgcc tagaaaacct 2750
ctcgcttcct cagcctccaa agtggagctg ggaggtagaa ggggaggaca ctgggtggtc 2810

tactgaccca actgggggca aaggtttgaa gacacagcct ccccgccag cccaagctg 2870
ggccgaggcg cgtttgtgta tatctgcctc cctgtctgt aaggagcagc gggaacggag 2930
cttcggagcc tcctcagtga aggtggtggg gctgccggat ctgggctgtg gggcccttgg 2990
gccacgctct tgaggaagcc caggctcgga ggaccctgga aaacagacgg gtctgagact 3050
gaaattgttt taccagctcc cagggtggac ttcagtgtgt gtatttgtgt aaatgggtaa 3110
aacaatttat ttctttttaa aaaaaaaaaa aaaaaaa 3147

```

<210> 4
 <211> 241
 <212> PRT
 <213> Homo Sapien

<400> 4
 Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1 5 10 15
 Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
 20 25 30
 Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
 35 40 45
 Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
 50 55 60
 His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
 65 70 75 80
 Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
 85 90 95
 Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
 100 105 110
 Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
 115 120 125
 Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
 130 135 140
 Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
 145 150 155 160
 Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
 165 170 175
 Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
 180 185 190
 Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
 195 200 205
 Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
 210 215 220
 Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
 225 230 235 240
 Val

<210> 5
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 5
 aatggccatg gcaggccagc ctcc

<210> 6

24

32

32

24

31

33

-10-

24745-1613

1	5	10	
<210> 12			
<211> 42			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Primer			
<400> 12			42
tctctcgaga aaagaattgt ccaaggaagg gaaacagcta tg			
<210> 13			
<211> 39			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Primer			
<400> 13			39
atagcggccg cacactacat accagtcttt gaggcaatc			
<210> 14			
<211> 11			
<212> PRT			
<213> Homo sapien			
<400> 14			
Lys Arg Ile Val Gln Gly Arg Glu Thr Ala Met			
1 5 10			
<210> 15			
<211> 2100			
<212> DNA			
<213> Homo sapien			
<220>			
<221> CDS			
<222> (45)...(1361)			
<223> MTSP7: full length cDNA			
<220>			
<221> CDS			
<222> (45)...(1361)			
<223> MTSP7: full length cDNA			
<400> 15			56
agatcagatg gcgactgaat agaagctgcc ccagtcctgg gttc atg atg tac aca			
		Met Met Tyr Thr	
		1	
cct gtt gaa ttt tca gaa gct gaa ttc tca cga gct gaa tat caa aga			104
Pro Val Glu Phe Ser Glu Ala Glu Phe Ser Arg Ala Glu Tyr Gln Arg			
5 10 15 20			
aag cag caa ttt tgg gac tca gta cgg cta gct ctt ttc aca tta gca			152
Lys Gln Gln Phe Trp Asp Ser Val Arg Leu Ala Leu Phe Thr Leu Ala			
25 30 35			

24745-1613

att gta gca atc ata gga att gca att ggt att gtt act cat ttt gtt Ile Val Ala Ile Ile Gly Ile Ala Ile Gly Ile Val Thr His Phe Val 40 45 50	200
gtt gag gat gat aag tct ttc tat tac ctt gcc tct ttt aaa gtc aca Val Glu Asp Asp Lys Ser Phe Tyr Tyr Leu Ala Ser Phe Lys Val Thr 55 60 65	248
aat atc aaa tat aaa gaa aat tat ggc ata aga tct tca aga gag ttt Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser Ser Arg Glu Phe 70 75 80	296
ata gaa agg agt cat cag att gaa aga atg atg tct agg ata ttt cga Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser Arg Ile Phe Arg 85 90 95 100	344
cat tct tct gta ggc ggt cga ttt atc aaa tct cat gtt atc aaa tta His Ser Ser Val Gly Gly Arg Phe Ile Lys Ser His Val Ile Lys Leu 105 110 115	392
agt cca gat gaa caa ggt gtg gat att ctt ata gtg ctc ata ttt cga Ser Pro Asp Glu Gln Gly Val Asp Ile Leu Ile Val Leu Ile Phe Arg 120 125 130	440
tac cca tct act gat agt gct gaa caa atc aag aaa aaa att gaa aag Tyr Pro Ser Thr Asp Ser Ala Glu Gln Ile Lys Lys Lys Ile Glu Lys 135 140 145	488
gct tta tat caa agt ttg aag acc aaa caa ttg tct ttg acc ata aac Ala Leu Tyr Gln Ser Leu Lys Thr Lys Gln Leu Ser Leu Thr Ile Asn 150 155 160	536
aaa cca tca ttt aga ctc aca cct att gac agc aaa aag atg agg aat Lys Pro Ser Phe Arg Leu Thr Pro Ile Asp Ser Lys Lys Met Arg Asn 165 170 175 180	584
ctt ctc aac agt cgc tgt gga ata agg atg aca tct tca aac atg cca Leu Leu Asn Ser Arg Cys Gly Ile Arg Met Thr Ser Ser Asn Met Pro 185 190 195	632
tta cca gca tcc tct tct act caa aga att gtc caa gga agg gaa aca Leu Pro Ala Ser Ser Ser Thr Gln Arg Ile Val Gln Gly Arg Glu Thr 200 205 210	680
gct atg gaa ggg gaa tgg cca tgg cag gcc agc ctc cag ctc ata ggg Ala Met Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln Leu Ile Gly 215 220 225	728
tca ggc cat cag tgt gga gcc agc ctc atc agt aac aca tgg ctg ctc Ser Gly His Gln Cys Gly Ala Ser Leu Ile Ser Asn Thr Trp Leu Leu 230 235 240	776
aca gca gct cac tgc ttt tgg aaa aat aaa gac cca act caa tgg att Thr Ala Ala His Cys Phe Trp Lys Asn Lys Asp Pro Thr Gln Trp Ile 245 250 255 260	824
gct act ttt ggt gca act ata aca cca ccc gca gtg aaa cga aat gtg Ala Thr Phe Gly Ala Thr Ile Thr Pro Pro Ala Val Lys Arg Asn Val 265 270 275	872
agg aaa att att ctt cat gag aat tac cat aga gaa aca aat gaa aat	920

-13-

24745-1613

<400> 16
 Met Met Tyr Thr Pro Val Glu Phe Ser Glu Ala Glu Phe Ser Arg Ala
 1 5 10 15
 Glu Tyr Gln Arg Lys Gln Gln Phe Trp Asp Ser Val Arg Leu Ala Leu
 20 25 30
 Phe Thr Leu Ala Ile Val Ala Ile Ile Gly Ile Ala Ile Gly Ile Val
 35 40 45
 Thr His Phe Val Val Glu Asp Asp Lys Ser Phe Tyr Tyr Leu Ala Ser
 50 55 60
 Phe Lys Val Thr Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser
 65 70 75 80
 Ser Arg Glu Phe Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser
 85 90 95
 Arg Ile Phe Arg His Ser Ser Val Gly Gly Arg Phe Ile Lys Ser His
 100 105 110
 Val Ile Lys Leu Ser Pro Asp Glu Gln Gly Val Asp Ile Leu Ile Val
 115 120 125
 Leu Ile Phe Arg Tyr Pro Ser Thr Asp Ser Ala Glu Gln Ile Lys Lys
 130 135 140
 Lys Ile Glu Lys Ala Leu Tyr Gln Ser Leu Lys Thr Lys Gln Leu Ser
 145 150 155 160
 Leu Thr Ile Asn Lys Pro Ser Phe Arg Leu Thr Pro Ile Asp Ser Lys
 165 170 175
 Lys Met Arg Asn Leu Leu Asn Ser Arg Cys Gly Ile Arg Met Thr Ser
 180 185 190
 Ser Asn Met Pro Leu Pro Ala Ser Ser Ser Thr Gln Arg Ile Val Gln
 195 200 205
 Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
 210 215 220
 Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu Ile Ser Asn
 225 230 235 240
 Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn Lys Asp Pro
 245 250 255
 Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro Pro Ala Val
 260 265 270
 Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr His Arg Glu
 275 280 285
 Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr Gly Val Glu
 290 295 300
 Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser Ser Ile Lys
 305 310 315 320
 Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly Ser Ile Val
 325 330 335
 Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg Val Glu Thr
 340 345 350
 Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp Gly Leu Ile
 355 360 365
 Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys Ile Asp Ala
 370 375 380
 Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn His Asp Ile
 385 390 395 400
 Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys Ala Leu Pro
 405 410 415
 Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg Asp Trp Ile
 420 425 430
 Ala Ser Lys Thr Gly Met
 435

<210> 17
 <211> 702
 <212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (1)...(702)

<223> Nucleotide sequence encoding Protease Domain

<400> 17

att gtc caa gga agg gaa aca gct atg gaa ggg gaa tgg cca tgg cag	48
Ile Val Gln Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln	
1 5 10 15	
gcc agc ctc cag ctc ata ggg tca ggc cat cag tgt gga gcc agc ctc	96
Ala Ser Leu Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu	
20 25 30	
atc agt aac aca tgg ctg ctc aca gca gct cac tgc ttt tgg aaa aat	144
Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn	
35 40 45	
aaa gac cca act caa tgg att gct act ttt ggt gca act ata aca cca	192
Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro	
50 55 60	
ccc gca gtg aaa cga aat gtg agg aaa att att ctt cat gag aat tac	240
Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr	
65 70 75 80	
cat aga gaa aca aat gaa aat gac att gct ttg gtt cag ctc tct act	288
His Arg Glu Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr	
85 90 95	
gga gtt gag ttt tca aat ata gtc cag aga gtt tgc ctc cca gac tca	336
Gly Val Glu Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser	
100 105 110	
tct ata aag ttg cca cct aaa aca agt gtg ttc gtc aca gga ttt gga	384
Ser Ile Lys Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly	
115 120 125	
tcc att gta gat gat gga cct ata caa aat aca ctt cgg caa gcc aga	432
Ser Ile Val Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg	
130 135 140	
gtg gaa acc ata agc act gat gtg tgt aac aga aag gat gtg tat gat	480
Val Glu Thr Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp	
145 150 155 160	
ggc ctg ata act cca gga atg tta tgt gct gga ttc atg gaa gga aaa	528
Gly Leu Ile Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys	
165 170 175	
ata gat gca tgt aag gga gat tct ggt gga cct ctg gtt tat gat aat	576
Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn	
180 185 190	
cat gac atc tgg tac att gta ggt ata gta agt tgg gga caa tca tgt	624
His Asp Ile Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys	
195 200 205	
gca ctt ccc aaa aaa cct gga gtc tac acc aga gta act aag tat cga	672

Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg
 210 215 220

gat tgg att gcc tca aag act ggt atg tag
 Asp Trp Ile Ala Ser Lys Thr Gly Met *
 225 230

702

<210> 18
 <211> 233
 <212> PRT
 <213> Homo sapien

<400> 18
 Ile Val Gln Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln
 1 5 10 15
 Ala Ser Leu Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu
 20 25 30
 Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn
 35 40 45
 Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro
 50 55 60
 Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr
 65 70 75 80
 His Arg Glu Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr
 85 90 95
 Gly Val Glu Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser
 100 105 110
 Ser Ile Lys Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly
 115 120 125
 Ser Ile Val Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg
 130 135 140
 Val Glu Thr Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp
 145 150 155 160
 Gly Leu Ile Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys
 165 170 175
 Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn
 180 185 190
 His Asp Ile Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys
 195 200 205
 Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg
 210 215 220
 Asp Trp Ile Ala Ser Lys Thr Gly Met
 225 230

<210> 19
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 19
 tctctcgaga aaagaattgt ccaaggaagg gaaacagcta tg

42

<210> 20
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 20

agatgagtct gggaggctaa ctctctggac tat

33

<210> 21

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 21

attcgcggcc gcctacatac cagtctttga ggcaat

35

<210> 22

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 22

atagtcaga gagttagcct cccagactca tct

33